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# 811 Pea cultivar and wheat residues affect carbon/nitrogen dynamics in pea-triticale

## 812 intercropping: a microcosms approach

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#### 823 Abstract

The underlying mechanisms by which legume cultivars contribute to nitrous oxide (N<sub>2</sub>O) generation 824 are poorly understood. The aim of the present study was to explore the effects of two pea cultivars 825 826 (Zero4 and Nitouche) intercropped with triticale, with or without wheat (Triticum aestivum) residues 827 incorporation, on soil C and N dynamics, on bacterial community structure and their links with N2O emissions. Monocrops and bare soil (no plant) treatments were used as an additional control in order 828 to account for the level of mineralisation between treatments. Changes in total C and N contents and 829 830 in some functionally-related soil pools (microbial biomass C and N, basal respiration, KClexchangeable ammonium and nitrate, potentially mineralizable N, DOC, ecophysiological indexes) 831 832 were followed throughout a 97-day microcosm experiment carried out on a loamy arable soil. ARISA community fingerprinting of soil extracted DNA and GHG emissions were carried out at 833 two key stages (pea flowering and harvest). The addition of residues to the soil resulted in only small 834 835 changes to the total C and N pools the Nitouche monocrop, which was found to have the highest potentially mineralisable N (13.4  $\mu$ g g<sup>-1</sup> 28d<sup>-1</sup>) of the treatments with added residue. The different 836 pea cultivar selectively affected N<sub>2</sub>O emissions, with highest emissions associated with the cultivar 837 Nitouche in the absence of residues. The two intercropping treatments of triticale/pea were 838 significantly different either with residues or without, especially the triticale/Zero 4 which had the 839 lowest values (356 g N<sub>2</sub>O-N ha<sup>-1</sup>). Similar patterns were also observed in below ground data. ARISA 840 analysis showed that monocropped legumes and the Triticale-based treatment clearly grouped on 841 separate clusters to the added residue treatment. We hypothesize that in pea-based intercrops 842 843 variations in carbon supply from different cultivars may contribute to differences in N<sub>2</sub>O emissions and thus influence the choice of suitable cultivars, to optimize nutrient cycling and sustainable crop 844 845 management.

# 846 Keywords

- 847 bacterial community structure, C and N pools, N<sub>2</sub>O emissions, pea-based intercropping, wheat
- 848 residues

#### 849 Introduction

Legume cropping offers opportunities to reduce GHG emissions from agriculture through their 850 851 ability to substitute inputs of mineral fertilisers with biologically fixed N (Rochette and Janzen 852 2005). However, legumes differ widely in the their contribution to N<sub>2</sub>O emissions and in some cases (particularly following residue incorporation) can still remain a significant source (Baggs et al., 853 854 2000; Bouwman et al., 2002). The cultivation of leguminous crops in agricultural systems can not only contribute to reducing the emission of nitrous oxide (N<sub>2</sub>O) but also increases the release and 855 856 the turnover of mineralisable N-containing compounds in soil (Rochette and Janzen 2005; Jensen et 857 al., 2010). Their ability to add external N to the plant-soil system is a distinct benefit on which crop 858 production systems can rely on in order to maintain the soil N supply at a sustained productive level (Watson et al., 2011). The amount of biologically fixed N supplied by legumes varies greatly from 859 860 tens to several hundred kilograms per ha per year and is strongly affected by the type and 861 environmental conditions (nitrate availability, temperature, soil wetness, and the availability of other nutrients). 862

863 Although symbiotic Rhizobium is believed to be able to produce N<sub>2</sub>O in root nodules there is a conflicting evidence regarding the magnitude of this process. In their early work, O'Hara and 864 865 Daniel (1985) suggested that rhizobial microorganisms are directly involved in the production of N<sub>2</sub>O by reduction of NO<sub>3</sub> occurring within the root nodules. However, it is likely that Rhizobium 866 867 species are not directly involved in the N<sub>2</sub>O production process, and that the root microflora also 868 plays an important role. Okubo et al. (2009) have shown that the rhizosphere community structure is significantly influenced by plant species and cultivar. It is also likely that this community 869 870 structure is influenced by environmental conditions. It has been shown that different nodulation 871 phenotypes contain different bacterial and fungal profiles in the stems and roots (Ikeda et al., 2008). However, the extent to which these phenotypes are associated with different emissions is unclear. In 872 the case of legumes, it has been suggested that N<sub>2</sub>O emission is primarily associated with 873 decomposition and turnover of root nodules (Inaba et al., 2009), which implies that differences in 874 875 the community structure and activity of root surface microorganisms may be responsible.

876 Understanding the contribution of legumes to N<sub>2</sub>O emissions in the wider environment is highly 877 dependent on developing an improved understanding of the underlying microbiology of the system 878 (Philippot et al., 2002). Many studies have been conducted involving legume based cropping 879 systems especially placed in intercrops or the growing of two or more species together at one time, 880 since, legume-based intercropping is able to provide several agro-ecological services: a more 881 efficient use of soil resources for plant growth due to a reduced competition for soil N (Hauggaard-882 Nielsen et al., 2003; Knudsen et al., 2004; Hauggaard-Nielsen and Jensen, 2005), an increased 883 water and nutrient use efficiency (Hauggaard-Nielsen et al., 2009a), a greater yield stability and 884 higher N concentration in cereal grain (Hauggaard-Nielsen et al., 2006, 2009b), a better control of 885 soil erosion (Inal et al., 2007), and an enhanced weed suppression and pest control (Liebman and Dyck, 1993; Corre-Hellou et al., 2011). Moreover, reduced N<sub>2</sub>O emissions from soil (Pappa et al., 886 887 2011) were also shown in leguminous intercrops. One more justification for intercropping 888 (especially pea-based) is the increased mineral N made available in the soil for the following crop (Pappa et al., 2011; Scalise et al., 2015). Finally, the legume cultivar has been shown to play an 889 890 important role in the cumulative N<sub>2</sub>O emissions of the agricultural systems, which also affects the 891 product intensities (Pappa et al., 2011), which are all the emissions divided by all saleable outputs.

The aim of this study was to explore the mechanisms responsible for N<sub>2</sub>O emissions from two legume species demonstrated by Pappa *et al.* (2011) by monitoring a number of soil chemical (pH; EC;  $C_{org}$ ; Nt; NH<sub>4</sub><sup>+</sup>-N; NO<sub>3</sub><sup>-</sup>-N; DOC), biochemical (MBC; R<sub>bas</sub>; C<sub>0</sub>, potentially mineralisable C; MBC/C<sub>org</sub>; *q*M, mineralisation coefficient; *q*CO<sub>2</sub>; *q*CO<sub>2</sub>/C<sub>org</sub> ratio; MBN; PMN, potentially mineralisable N) variables together with the bacterial community structure

by ARISA fingerprinting of soil extracted DNA, and GHGs emissions ( $N_2O$ ,  $CH_4$ ,  $CO_2$ ) in an arable soil as by a microcosms approach.

The present study tested the following three hypotheses: a) legume-based cropping systems and wheat residue incorporation can stimulate soil C and N cycling through the enhancement of the below-ground nutrient flow, b) GHG emissions from legume-based intercropping can be altered by 902 soil addition of wheat residues and c) even when showing a similar yield potential, the cultivar of a 903 same leguminous species can selectively influence the soil processes including the bacterial 904 community structure conditioned by the legume intercrop.

#### 905 **2. Materials and methods**

#### 906 2.1 Soil type and plant material

907 The soil used in the microcosm experiment was a loam collected from the Ap horizon (0-30 cm) 908 of an agricultural field cultivated under continuous winter wheat and located at the Bush Estate, Edinburgh, Scotland (55°52'17.46" N, 3°12'24.27" W). The main soil properties were: sand 42%, 909 silt 34%, clay 24%; bulk density  $1.2 \pm 0.1$  kg dm<sup>-3</sup>; pH<sub>H2O</sub> 6.19 ± 0.04; total organic C (C<sub>org</sub>) 34.27 910  $\pm 1.22$  g kg<sup>-1</sup>; total N (N<sub>t</sub>) 2.52  $\pm 0.08$  g kg<sup>-1</sup>; C:N ratio 13.62  $\pm 0.20$ ; NH<sub>4</sub><sup>+</sup> - N 3.75  $\pm 0.40$  mg kg<sup>-1</sup>; 911 NO<sub>3</sub><sup>-</sup> - N 7.64  $\pm$  0.50 mg kg<sup>-1</sup>; Olsen P 18.2  $\pm$  0.4 mg kg<sup>-1</sup>; extractable K 202.0  $\pm$  0.3 mg kg<sup>-1</sup>; 912 electric conductivity measured in a soil:water (1:2, w/v) mixture (EC<sub>1:2</sub> at 25°C)  $0.10 \pm 0.01$  dS m<sup>-1</sup>. 913 914 Following the winter wheat (Triticum aestivum) harvest (September 2011), residual straw was chopped to 2-4 mm and stored before being used for soil amendment. The soil for filling the 915 microcosms was collected before starting the experiment ( $3^{rd}$  October 2011), coarse sieved at < 4.7-916 917 mm particle size and brought to approximately 30% gravimetric water content. Seeds of two cultivars of spring pea (Pisum sativum L. cv. Nitouche and Pisum sativum L. cv. Zero4) were 918 919 provided by PGRO (UK); seeds of triticale (Triticum aestivum L. x Triticosecàle Wittm.) were 920 provided by APSOVSEMENTI s.p.a. (Pavia, I).

#### 921 2.2 Experimental set-up

The microcosm study was carried out at Scotland's Rural College (SRUC), in Edinburgh, between October 2011 and February 2012. Microcosm units consisted of 2.12 L polyvinyl chloride (PVC) pipes (25 cm height, 10.4 cm internal diameter) that had been closed at the base with an airtight seal using a sheet of Plexiglas<sup>®</sup>. A sampling point for the gas collection (a three-way tap) was placed at 23 cm depth from the surface of the microcosm. Microcosms were filled either with soil 927 (no residue addition) (unamended) or with a soil plus chopped wheat straw (400:1, w/w) mixture 928 (corresponding to a 6.3 t  $ha^{-1}$  addition rate at a field scale) (wheat residue addition) (amended).

The amount of soil needed was calculated by taking into account the microcosm volume (1867.92 cm<sup>3</sup>), the soil bulk density and the gravimetric water content in order to reach a waterfilled pore space (WFPS) equal to 28-32% that provides optimum conditions for biological activity in soil (FAO, 2001). WFPS was kept constant during the growing season by watering with a N-free artificial rainwater (Palmqvist and Dahlman, 2006) in order to maintain suitable conditions for plant growth and microbial processes without providing an external N addition.

Soon after filling (7<sup>th</sup> October 2011), each microcosm, four seeds were initially sown but only two plants, of the same species or one of each intercrop components, were kept after successful seed germination. For each level of soil amendment, the following six treatments compared different combinations of leguminous intercrops and the respective sole crop: i) Nitouche: monocrop of pea ev. Nitouche; ii) Zero4: monocrop of pea cv. Zero4; iii) Triticale: monocrop of Triticale; iv) Nitouche-Triticale: intercrop pea cv. Nitouche-Triticale; v) Zero4-Triticale: intercrop pea cv. Zero4-Triticale and vi) bare soil: unplanted microcosms were used as a control.

Since the scheduled samplings were destructive, the whole experiment was duplicated, giving a
total of 72 microcosms: (6 treatments) x (2 levels of amendment) x (2 samplings) x (3 replicates).
The microcosms were randomly arranged in a growth chamber and grown for a 97-day growing
period under controlled climatic conditions, as shown in Table 1.

#### 946 2.3Soil sampling and analysis

Soil samples were collected at three sampling times: at the beginning (pre-sowing), at pea flowering (62 days after sowing (DAS)) and at the pods filling pea stage (97 DAS), when the microcosms were destructively sampled for soil and plant collection. Each microcosm provided one rhizosphere sample (two samplings) and one bulk soil sample (three samplings). The rhizosphere soil was taken from the plant roots after the bulk of the soil had been removed. The rhizosphere soil was used for the molecular analysis and the bulk soil was used for the chemical and biochemical 953 characterization.

954 Soil chemical properties were determined according to standards methods recommended by the Soil Science Society of America (Sparks, 1996). Dissolved organic carbon (DOC) was extracted 955 with water (1:2 w/v, soil:water) after shaking (170 rpm, 30 min) at room temperature. The soil 956 957 slurries were then centrifuged (4300 rpm, 10°C, 10 min) and the recovered supernatant was filtered through a 0.45 µm Whatman GF/F membrane. DOC in the clean extract was finally measured using 958 959 an automated elemental OC analyzer (Rosemount-Dohrmann DC-80) (Jones et al., 2005) using a 960 perchlorate oxidation followed by detection of CO<sub>2</sub> by NIR spectroscopy. Inorganic-N (NO<sub>3</sub><sup>-</sup>-N and NH4<sup>+</sup>-N) was extracted with 1 M KCl (1:5, w/v, soil:solution) after shaking (220 rpm, 60 min) at 961 962 24°C. After the extraction, the soil slurries were centrifuged (4300 rpm, 10 min) and the clean supernatants recovered and stored at -20°C before analysis. Inorganic N was determined using a 963 continuous flow auto-analyser (SKALAR San<sup>++</sup>, BV, NL). 964

965 Microbial biomass C (MBC) and N (MBN) were determined following a chloroform fumigation-extraction (CFE) procedure according to Vance et al. (1987) and Brookes et al. (1985). 966 MBC was estimated using a conversion factor of  $K_{\rm EC} = 0.45$  (Joergensen, 1996) and MBN was 967 968 estimated using a conversion factor of  $K_{\rm EN} = 0.54$  (Joergensen and Mueller, 1996). Soil basal respiration was estimated by measuring CO2 emissions in sealed 1.5 L jars containing 20 g (dw 969 970 equivalent) soil samples and incubated in the dark at 24 °C. Gas samples were collected in preevacuated 22 ml vials and analysed by gas chromatography (Sparling, 1981). The cumulative CO<sub>2</sub>-971 C evolved after a 28-day incubation period (gas sampling was carried out after 1, 4, 7, 14, 21 and 28 972 973 days) was assumed as  $R_{bas}$ . The potentially mineralisable C (C<sub>0</sub>) was estimated by fitting the 28-day cumulative data to the first-order exponential function  $C_t=C_0$  (1-e<sup>-kt</sup>) (Riffaldi *et al.*, 1996). The best 974 fitting of the equation to the values experimentally obtained and estimates of C<sub>0</sub> and k parameters 975 976 for each curve of basal respiration were obtained by non-linear regression analysis using the Levenburg-Marquardt algorithm (Table Curve 2D v 5.01 software, SYSTAT software Inc.). 977 978 Potentially mineralisable N (PMN), resulting from net mineralization of active soil organic N 979 occurring during the 28-day incubation period for  $R_{bas}$  determination, was estimated as the 980 cumulative inorganic soil N after 28 days *minus* the inorganic soil N at 0 day (Drinkwater *et al.*, 981 1996). The following soil eco-physiological indices were then calculated: the microbial quotient 982 (MBC/C<sub>org</sub>), the metabolic quotient (*q*CO<sub>2</sub>), the mineralization coefficient (*q*M=R<sub>bas</sub>/C<sub>org</sub>) and the 983 *q*CO<sub>2</sub>/C<sub>org</sub> ratio (Dilly *et al.*, 2001; Mocali *et al.*, 2009).

984 DNA extraction from both rhizosphere and bulk soil were undertaken by ball milling samples to 985 achieve physical lysis followed by a CTAB-buffer extraction method as described by Brierley et al. 986 (2009). DNA extracts were purified from any humic acids by passing them through micro Bio-spin columns loaded with polyvinylpyrrolidone (PVP). DNA yield and quality were quantified by a 987 988 spectrophotometer (ND-1000). Automated ribosomal intergenic spacer analysis (ARISA) was 989 with end-point PCR technique using carried an the primer system 1406f (5'-TGYACACCGCCCGT-3') and 23Sr (5'-GGGTTBCCCCATTCRG-3'). The PCR reaction 990 mixture was prepared with GoTag<sup>®</sup> Green Master Mix (Promega), 2 µl of template DNA (ca 20 ng), 991 992 0.5 µM of each primer, and sterile deionised water to a final volume of 25 µl. In the negative 993 control, the tDNA was substituted with the same volume of nuclease-free water (Promega). PCR 994 running conditions started with a single denaturation step of 94 °C for 3 min, to activate the 995 HotStart enzyme, followed by 29 thermal cycles consisting of a denaturation step at 94 °C for 45 s, 996 an annealing step at 55 °C for 1 min, and an elongation step at 72 °C for 2 min, followed by a final primer extension at 72 °C for 7 min and cooling to 4 °C. Capillary electophoresis with peaks 997 998 ranging from 50-bp to 1,050-bp was carried out using an DNA 7500 assays on the Agilent 2100 999 Bioanalyzer (Analysis Software 2100, Agilent Technologies, Böblingen, D) according to manufacturer instructions. Electropherograms were imported into BioNumerics<sup>®</sup> 7.0 software 1000 1001 package (AppliedMaths, Sint-Martens-Latem, B) as a 2D gel image for further analysis.

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#### 1003 2.4 Greenhouse gas monitoring

1004 Emissions of  $N_2O$ , carbon dioxide ( $CO_2$ ) and methane ( $CH_4$ ) from the microcosm units were

1005 measured following three gas sampling strategies: soil surface emissions, deep layer emissions (23 1006 cm) and respiration from roots. Surface gas monitoring started 12 days after sowing and was 1007 repeated (twice a week) across the entire experimental period by using the closed chamber 1008 technique (Smith et al., 1995). During the gas emission measurements, the microcosms were 1009 covered by a 26-cm-tall chamber for 40-60 minutes before collecting 40 ml gas samples in a portable pre-evacuated 22-ml-glass vial (Scott et al., 1999). For baseline corrections two air 1010 1011 samples from the growing chamber atmosphere were collected at each sampling time. Gas sampling from deep soil layers started 38 days after sowing (14<sup>th</sup> November 2011) to allow time for the roots 1012 1013 to grow throughout the microcosm and was repeated twice a week for three weeks. Gaseous 1014 emissions from legume roots collected after the microcosm destructive sampling (see below) were 1015 measured as described by Inaba et al. (2009). Shortly after the harvest, unwashed legume roots were 1016 placed into a 320 ml air-tight glass jars; 0 and 10 min after sealing, a 40-ml-gas sample was 1017 collected from the glass jar and immediately transferred in a pre-evacuated 22 ml glass vial. All gas 1018 samples were stored (maximum 1 day) in a controlled temperature room before any analysis. Amounts of N<sub>2</sub>O, CO<sub>2</sub> and CH<sub>4</sub> of collected air samples were analyzed using an Agilent 6890 gas 1019 1020 chromatograph equipped with a 1.8 m Propak-N column and an electron capture detector (for N<sub>2</sub>O) 1021 and flame ionisation detector (for CH<sub>4</sub>). Certified high purity gas standards of known concentration 1022 were used for calibration. The conversion of peak areas to daily gaseous emissions was carried out 1023 in accordance with standard procedures (de Kleine and Harvey, 2013). In addition, greenhouse gas emission intensities were expressed per unit of product (all emissions divided by all saleable 1024 1025 outputs. Also the Global Warming Potential (GWP) of each gas was calculated using coefficients of 1 for  $CO_2$ , 25 for  $CH_4$  and 298 for  $N_2O$ . 1026

#### 1027 2.5 Plant sampling and analysis

At pea flowering (62 DAS) and pod filling (97 DAS), the microcosms were destructively sampled, plants were gently removed from the microcosm soil and separated into shoot and root fractions. Shoot fresh weight was immediately recorded, whereas the root system was initially used 1031 for measuring the  $N_2O$  emissions (legumes only). The above ground biomass results were used for 1032 the emission intensities calcilations.

#### 1033 *2.6 Statistics*

1034 Soil variables were firstly checked for deviations from normality (Shapiro Wilk's test) and 1035 homogeneity of within-group variances (Levene's test). The block effect in the experimental design was not significant (P > 0.05) and the data were subjected to the following statistical analyses. A 1036 1037 three-way analysis of variance (ANOVA) (treatment (T) x amendment (A) x time (Ti)), indicated in 1038 Figs. 1, 2 and 4 and in Table 2 as F-values and corresponding P-values, was performed in order to 1039 highlight the main effect of sampling time, crops, level of amendment and their interactions on measured soil variables. Significant effects due to treatment (T), amendment (A), and their 1040 1041 interaction presented in Tab. 4 were estimated by a two-way ANOVA. Multiple pairwise comparison of means were assessed by Tukey's HSD (Honestly Significant Difference) test at P <1042 1043 0.05 level of significance. Chemical and biochemical data were also analysed by principal 1044 component analysis (PCA) with no rotation with data from three different stages (pre-sowing, flowering and harvest) (Table 3 and 4). Statistical analyses were run using the Systat 11.0 software 1045 1046 (SYSTAT Software Inc., Erkrath, D). Graphs were drawn by using the SigmaPlot 10.0 software 1047 (SYSTAT Software Inc.). Dendrograms of hierarchical classification of ARISA profiles were 1048 generated by cluster analysis using the unweighed pair-group method with arithmetic averages 1049 (UPGMA) based on Dice similarity coefficient as suggested by Rademaker et al. (1999).

#### 1050 **3. Results**

#### 1051 *3.1 Soil C pools*

Soil carbon pools showed variable responses to the addition of plant residues and the presence of different crop cultivars during the experiment. The addition of wheat residues in the microcosm soils caused some significant reductions in the amount of the total organic carbon ( $C_{org}$ ) (Table 2), although residue incorporation affected the  $C_{org}$  differently in treatments over time. In particular, in unamended soils,  $C_{org}$  values remained close to the initial values; whereas following wheat residue addition, a contrasting affect was observed in  $C_{org}$  content between monocropped treatments were found to have the highest  $C_{org}$  concentrations. In bare soil  $C_{org}$  slightly declined, whereas it remained practically unaffected in amended ones.

Dissolved organic carbon (DOC) varied in response to residue addition levels and sampling stages (Fig. 1). The presence of the intercrops increased the concentrations of DOC at harvest. Without residues addition, no significant difference was observed between treatments at any sampling stage; whereas following wheat residue addition the Zero4 treatment showed a significant increase (P < 0.001) from pre-sowing (36.9 µg g<sup>-1</sup>) to harvest (64.1 µg g<sup>-1</sup>). On average, DOC increased over time from an initial value of 33.2 (or 37.3) to 48.2 (or 50.5) µg g<sup>-1</sup> in unamended (or amended) microcosms soil, including the bare soil which showed an increasing trend over time.

In unamended microcosms, mean soil basal respiration, R<sub>bas</sub>, values were higher than pre-1067 sowing at both flowering and harvest stage (respectively 778.9 and harvest 807.4 µg CO<sub>2</sub>-C g<sup>-1</sup> 28 d<sup>-1</sup> 1068 <sup>1</sup>) and there was no significant effect due to the crop treatment (Fig. 1). However, residue 1069 amendment strongly influenced (P < 0.05) the CO<sub>2</sub> emission of treatments at the harvest stage, 1070 which ranged between 553.5 (bare soil) and 1042.6  $\mu$ g CO<sub>2</sub>-C g<sup>-1</sup> 28 d<sup>-1</sup> (Nitouche monocropping): 1071 1072 the Nitouche solo crop showed higher basal respiration than those at beginning of the experiment (from 721.7 to 1042.6  $\mu$ g CO<sub>2</sub>-C g<sup>-1</sup> 28 d<sup>-1</sup>), whereas in the bare soil R<sub>bas</sub> decreased by 1073 approximately 20% (from 664.6 to 553.5 µg CO<sub>2</sub>-C g<sup>-1</sup> 28 d<sup>-1</sup>). Estimates of the potentially 1074 mineralisable carbon (C<sub>0</sub>) followed the same general trend as those of R<sub>bas</sub>, even though some of the 1075 1076 experimental factors lost their significance (Fig. 1). It is noteworthy that C<sub>0</sub> displayed a time-1077 dependent fluctuation with particularly high C mineralization from Triticale (differing from R<sub>bas</sub>) 1078 and Nitouche monocrops.

1079 Microbial biomass carbon (MBC) was strongly affected by treatments with statistically 1080 significant responses to all the experimental factors (Fig. 1). In general the MBC increased during 1081 the cropping season, in spite of residue amendment: from an initial 79.0 (or 75.5) to final 191.4 (or 1082 243.6)  $\mu$ g C g<sup>-1</sup> in unamended (or amended) soil microcosms. In soils with no wheat residue 1083 addition, MBC showed a large increase in the presence of legume-based treatments either in 1084 monocropped - from mean initial 79.1 to final 209.3  $\mu$ g C g<sup>-1</sup> (approximately +265%) - or 1085 intercropped legumes - from initial 75.5 to final 233.8  $\mu$ g C g<sup>-1</sup> (approximately +310%). An 1086 opposite affect was observed in residue amended soils: the MBC increase was generally lower 1087 under intercropping (+290%) than in monocropping (+390%) as compared with the starting value of 1088 75.7  $\mu$ g C g<sup>-1</sup>.

#### 1089 *3.2 Soil N pools*

1090 Time and time x amendment were the only factors that significantly affected the variability of total nitrogen content (Nt) in microcosms soils (Table 2). In fact, Nt content decreased across the 97-1091 1092 day experimental period with differing trends, but reaching similar values at the harvest stage (2.09) and 2.01 g kg<sup>-1</sup> for unamended and amended, respectively) (data not shown). Across the 1093 experimental period, the extractable NH<sub>4</sub><sup>+</sup>-N did not differ significantly in any of the treatments 1094 1095 (Fig. 2); however, the amount of soil nitrate showed marked time-dependent fluctuations and was significantly different among treatments (P < 0.001). Crop growth markedly affected the dynamics 1096 1097 of soil nitrate-N, which became greatly depleted at the flowering stage in all planted microcosms. 1098 An increased release of nitrate was observed at the latest stage, also mirrored by a decline in the 1099 ammonium-N content, yet regulated by the decaying wheat residues (Fig. 2).

1100 The potentially mineralisable nitrogen (PMN) was affected by all the experimental factors and 1101 their interactions (Fig. 2). In general, PMN demonstrated a clear decrease from pre-sowing onward. 1102 At the flowering stage, PMN in the bare soil treatment was significantly higher (P < 0.01) than the 1103 treatments with no residue addition. It was noteworthy that, at the harvest stage, PMN was significantly affected by residue amendment, even though at a different level (P < 0.05 and P < 0.051104 0.001, respectively). Specifically, Nitouche monocropping increased the PMN by three times from 1105 the flowering stage reaching the highest value of 13.4  $\mu$ g g<sup>-1</sup> 28d<sup>-1</sup> in microcosms packed without 1106 1107 addition of wheat residues. All the remaining cropping treatments showed a small non-significant 1108 increase, but the bare soil retained similar values (10.81  $\mu$ g g<sup>-1</sup> 28 d<sup>-1</sup>). Further, in amended soils, 1109 there was a significant increase in the Triticale - Zero4 intercropping from the flowering (5.8  $\mu$ g g<sup>-1</sup> 1110 28 d<sup>-1</sup>) to the harvest stage (12.3  $\mu$ g g<sup>-1</sup> 28 d<sup>-1</sup>).

All experimental factors and their interactions statistically influenced the microbial biomass N (P < 0.001). In unamended microcosms, MBN moderately (intercrops) or strongly (monocrops) increased over time, with the exception of the bare soil treatment where it decreased from the beginning of the experimental period (14.6 µg N g<sup>-1</sup>) by approx. 40% (from 14.6 to 8.8 µg N g<sup>-1</sup>). In contrast, in residue amended soils, the unplanted soil showed MBN values statistically comparable to other cropping treatments: as a whole MBN increased by approx. 70%, from initial 17.0 to final 28.8 µg N g<sup>-1</sup> (Fig. 2).

#### 1118 3.3 Soil ecophysiological indices and C-to-N ratios

The mineralization coefficient (*q*M) was statistically influenced by the amendment level (P < 0.001), time (P < 0.001) and their interactions (Fig. 3). In unamended soils, the mineralization coefficient values showed a slight increase, on average from 16.79 µg CO<sub>2</sub>–C mg<sup>-1</sup> C<sub>org</sub> (pre-sowing stage) to 24.35 µg CO<sub>2</sub>–C mg<sup>-1</sup> C<sub>org</sub> (harvest sampling). In microcosms added with wheat residues, it showed an opposite trend for Zero4, Triticale and bare soil, which showed the major decline (from 25.14 µg CO<sub>2</sub>–C mg<sup>-1</sup> C<sub>org</sub> to 18.80 µg CO<sub>2</sub>–C mg<sup>-1</sup> C<sub>org</sub>).

1125 The metabolic quotient ( $qCO_2$ ) was significantly (P < 0.001) affected only by time, level of soil 1126 amendment and their interaction (Fig. 3). Microcosms at both level of amendment showed a decrease in the values of the  $qCO_2$  towards the end of the experiment, which was stronger in the 1127 amended soil due to the higher average values it showed in the pre-sowing stage (1.11 and 2.57 µg 1128 CO<sub>2</sub>-C µg<sup>-1</sup> MBC d<sup>-1</sup> respectively for unamended and amended). The largest decrease was 1129 registered in the Nitouche pure culture (from 2.69 to 0.19  $\mu$ g CO<sub>2</sub>–C  $\mu$ g<sup>-1</sup> MBC d<sup>-1</sup>). The *q*CO<sub>2</sub>/C<sub>oro</sub> 1130 ratio was also statistically influenced by time (P < 0.001), level of soil amendment (P < 0.001) and 1131 their interactions (Fig. 3). However, in amended microcosms, the  $qCO_2/C_{org}$  ratio clearly decreased 1132 1133 in all treatments from pre-sowing to harvest stage.

1134 The microbial quotient (MBC/C<sub>org</sub>) was strongly (P < 0.001) affected by all the experimental 1135 factors (Fig. 3). MBC/C<sub>org</sub> varied consistently during the experimental period and showed a marked 1136 increase at the harvest stage in all treatments at both amendment levels. The bare soil treatment 1137 always showed the lowest value within each sampling time, reaching its minimum at the flowering 1138 stage in residue amended microcosms (2.09 µg MBC mg<sup>-1</sup> C<sub>org</sub>).

#### 1139 *3.4 Soil pH and electrical conductivity*

1140 The three-way ANOVA revealed that wheat residue addition was the main factor affecting the 1141 variability of pH data (P < 0.001), which were generally higher in the amended soil (Table 2). There 1142 were also a time-dependent fluctuations (P < 0.01) together with significant effects of the 1143 amendment x time, and amendment x time x treatment interactions (P < 0.001). However, the pH 1144 varied between a narrow range comprised between 6.12 (unamended bare soil at flowering) and 6.37 (amended triticale at flowering), and significant differences among treatments were only 1145 1146 noticed at the flowering and the harvest stages in the unamended soil with the Nitouche monocrop 1147 and bare soil having, respectively, the highest (6.39) and the lowest value (6.10).

The electrical conductivity (EC<sub>1:2</sub>) varied between 0.10 and 0.18 dS  $m^{-1}$  and was significantly 1148 1149 affected by most of the experimental factors and their interactions (Table 2). It was noticeable that the triticale-based treatments showed higher  $EC_{1:2}$  values than the leguminous sole treatments at 1150 1151 both flowering and harvest stages: this finding was only observed in unamended, but not in the 1152 amended microcosms, and this was especially true for all crop-based treatments where EC remained 1153 almost constant over time. In the bare soil, the lowest EC was found in unamended treatments (~0.10 dS m<sup>-1</sup>); whereas following wheat residues addition it increased considerably at flowering 1154 and harvest stage, respectively to 0.18 and 0.15 dS m<sup>-1</sup>. 1155

#### 1156 3.5 Multivariate analysis

1157 According to the eigenvalue > 1.0 criterion only five principal components could be selected. The 1158 first two principal components PC1 (eigenvalue 5.37) and PC2 (eigenvalue 2.79) explained a large 1159 portion (33.55 and 17.44%, respectively) of the total variance. The following three components PC3 1160 (eigenvalue 2.17), PC4 (eigenvalue 1.35) and PC5 (eigenvalue 1.06) accounted for 13.54, 8.43 and 1161 6.63% of total variance, respectively. Since the first two components taken together explained as 1162 much as 50.98% of the total variance, we focused on them (Table 3). Firstly, it is worth noting that 1163 PC1 was primarily weighed by either C-related functional variables (DOC, qM, R<sub>bas</sub>, MBC and MBC/ Corg) or N-related variables (PMN and Nt). It was also found that PC2 was primarily affected 1164 by one of the most dynamic N pools in soil:  $NH_4^+$ -N, which was also directly related to  $aCO_2$  and 1165 1166 qCO<sub>2</sub>/C<sub>org</sub>. On the other hand MBN was the only variable affecting PC3. Moreover, PC4 was weighed by Corg and pH. Whereas, in PC5 PMC was the only soil variable showing a loading factor 1167 1168 close to the reference threshold value (0.60). In the ordination biplot of Factor 1 vs Factor 2, soil 1169 samples from the differing treatments appeared in most cases well separated at least in three main 1170 groups along the PC axis 1 (functional C variables and N-related properties): triticale 1171 monocropping, Nitouche - Triticale intercropping and, surprisingly, a rather broad group including 1172 all the other crop treatments plus the bare soil. On the other hand, the two leguminous monocrops 1173 were clearly separated along the PC axis 2 (Fig. 4A).

1174 The two first principal components PC1 (eigenvalue 5.21) and PC2 (eigenvalue 2.92) expressed a 1175 somewhat large portion (32.59 and 18.22%, respectively) of the total variance. The following three 1176 components PC3 (eigenvalue 2.04), PC4 (eigenvalue 1.46) and PC5 (eigenvalue 1.22) accounted 1177 for 12.77, 9.14 and 7.60% of total variance, respectively. Once again, we focused on the first two PCs as they explained as much as half of the variance (50.81%) (Table 4). PC1 was primarily 1178 1179 weighed by either C-related functional variables (MBC, MBC/C<sub>org</sub>, qCO<sub>2</sub>/C<sub>org</sub>, qCO<sub>2</sub> and DOC) or 1180 N-related variables (MBN, PMN and N<sub>t</sub>). PC2 was primarily affected by some C-related functional 1181 variables (R<sub>bas</sub>, qM and C<sub>0</sub>) and NO<sub>3</sub><sup>-</sup>-N. C<sub>org</sub> was the only variable affecting PC3. EC was the only 1182 variable affecting PC4.. In the ordination biplot of Factor 1 vs Factor 2, soil samples from the 1183 amended microcosms were rather scattered onto the plot: the two intercropping combinations were 1184 closely associated, whereas the two leguminous monocrops were not. The bare soil was well separated from the other treatments. Noticeably, among the chemical and biochemical soil variables,  $NO_3^-$ -N and C (C<sub>0</sub>) exerted a primary role in separating the treatments along the PC2 axis (Fig. 4B).

#### 1188 *3.6 ARISA analysis*

1189 The molecular structure of the bacterial communities profiles were characterized by the number 1190 and length distribution of major bands which, in spite of treatments and residue levels, were observed in a fragment size range from 200 to 1000 bp, and showed a clear diversity between levels 1191 1192 of residue. In particular, regardless of the growth stage, residues addiction in soils appeared to 1193 enhance the difference in groups allowing the monocropped legumes and Triticale-based treatment 1194 to clearly group on separate clusters (~78%; Fig. 5). On the contrary, in the no-residue soils, the 1195 treatment-dependent communities did not clearly align on the endemic axis, not allowing the clusters to present a clear pattern. The only clear difference was between bare soil and other 1196 1197 treatments, which showed a level of similarity of approximately 73%.

#### 1198 *3.7 Greenhouse gases (GHGs) emissions*

1199 Nitrous oxide emissions from the amended treatments were lower in comparison to the unamended 1200 soils (P < 0.001). In the amended treatments, the emissions started to pick up after 60 days of the 1201 start of the experiment with the unplanted treatment having the highest emissions (81.25 g N<sub>2</sub>O-N 1202 ha<sup>-1</sup> day<sup>-1</sup>). In the unamended treatments, the emissions were higher (P < 0.05) in the Triticale 1203 monocrop and Triticale/Nitouche treatments including also the no plant treatment from 30 days 1204 after the seeding.

The cumulative values of N<sub>2</sub>O were higher in the unamended treatments at 82 days. The bare soil treatment had the highest emissions in both treatments (4319 and 1430 g N<sub>2</sub>O-N ha<sup>-1</sup> in unamended and amended, respectively). In the microcosms with crop, the Triticale/Nitouche treatment had the highest (3677 g N<sub>2</sub>O-N ha<sup>-1</sup>) and the Triticale/Zero 4 the lowest (356 g N<sub>2</sub>O-N ha<sup>-1</sup>) emissions in unamended soils (P < 0.001). In the amended treatments, the cumulative emissions were generally

1210 very low, and even showed consumption of N<sub>2</sub>O (negative values) with similar patterns in the unamended soils (Triticale/Nitouche: 243 g N<sub>2</sub>O-N ha<sup>-1</sup> and Triticale/Zero4: -550 g N<sub>2</sub>O-N ha<sup>-1</sup>) 1211 1212 (Table 5). Below ground N<sub>2</sub>O emissions showed a similar pattern between amendment levels during 1213 the experimental period. However, the concentration of N<sub>2</sub>O was ten times greater from the no 1214 residue treatment in comparison with the residue (P < 0.001). The bare soil treatment had the 1215 highest average values (19.70 ppm and 1.95 ppm for the no residue and residue, respectively) followed by the Triticale/Nitouche treatment (2.56 and 1.30 ppm for the unamended and amended, 1216 1217 respectively) (Table 5).

1218 Cumulative CO<sub>2</sub> emissions were highest in the Zero 4 treatment (2511 kg CO<sub>2</sub>-C ha<sup>-1</sup>) in 1219 unamended soils and the Nitouche (2790 kg CO<sub>2</sub>-C ha<sup>-1</sup>) under residue addition (Table 5). The bare 1220 soil treatment had the highest average belowground concentration of CO<sub>2</sub> in both residue treatments 1221 during the experimental period (P < 0.001) (Table 5). Methane emissions were low during the 1222 experimental period for both level of amendment without (Table 5).

Emission intensities presented in this paper include the cumulative  $N_2O$  measurements (84 out of 97 days) for the total biomass produced within this time providing an index of the effectiveness of mitigation. In the residue treatment, the Triticale/Zero4 had the lowest emission intensities of all the treatments (-393 g N<sub>2</sub>O t biomass<sup>-1</sup>). N<sub>2</sub>O intensities were not significant different for the no residue treatment (Table 6).

#### **4. Discussion**

The results obtained from this study provide new insights into the interrelated effects of leguminous crops on the chemical and biochemical properties of soil and highlights the important differences in C and N cycling associated with pea-based intercropping and wheat residue incorporation.

#### 1233 4.1 Soil chemical properties

1234 Even in simplified ecosystems such as microcosms, soil organic carbon can be considered one of

the most important indicators of soil quality because of its important role in the maintenance of soil
structure, microorganisms and nutrient cycling (Aalders *et al.*, 2009).

Soil incorporation of wheat residues slightly reduced the total organic carbon ( $C_{org}$ ), which 1237 1238 appeared noticeable in the ANOVA analysis but resulted negligible impacts in the principal 1239 component analysis either with or without residue addition. Indeed, it could be anticipated that total 1240 soil organic matter, would not respond rapidly to environmental changes, unless major amendments are made (Powlson et al., 1987). However, mixing occurring during the establishment of the 1241 1242 experimental units was expected to alter soil C dynamic and enhance rates of soil organic matter 1243 degradation, thus leading to a so-called tillage effect (Linsler et al., 2013; Tortorella and Gelsomino, 1244 2011). The observation that soils receiving residue inputs were associated with lower organic C and 1245 N pools would indicate that the addition of residues had stimulated the microbial populations and 1246 increased the decomposition of preexisiting organic matter through a priming effect (Kuzvakov 1247 2002). This increased degradation activity not only influenced the carbon but also the nitrogen 1248 cycling, which is functionally interconnected in soil, and thus resulted in a more striking variation 1249 in N<sub>t</sub> than in the C<sub>org</sub>.

Even if major changes in total organic carbon content may be difficult to detect over a short-term experiment (Haynes, 1999), the responses of more labile fractions of soil organic carbon, namely dissolved organic carbon (DOC), are much more sensitive to soil management than total soil organic matter (Silveira, 2005). This fraction markedly influences soil chemical, biological and physical properties, as a primary source of mineralizable C, N, P, and S (Haynes, 2000) and it has been proposed as an indicator of the size of the available C pool to soil microorganisms (Boyer and Groffman, 1996).

1257 Through their exudates, plant root systems represents a major source of C flow entering the soil 1258 and stimulating the microbial process of immobilisation/release of soluble organic compounds 1259 forming the DOC pool in soil (Paterson, 2003; Paterson *et al.*, 2007). In fact, the quality and 1260 amount of rhizodeposition released from the legumes root systems could explain the high significance showed by the crop factor on the variability of this parameter in this study (Fustec *et*  $al_{.,2010}$ ).

The addition of plant residues and fresh organic compounds through rhizodepositions most often results in a net N immobilisation phase followed by a net re-mineralisation phase. In our study, lower amounts of inorganic N were observed in the treatment with wheat residue addition than in the corresponding unamended treatment. Wheat residue incorporation seems to have enhanced net N immobilization, although N mineralization was promoted in presence of the legume treatment at the end of the incubation period.

The significant difference between amendment levels and crop presence shown suggests a different effect of faunal activity on residues. This could be due to increased available N in soil, which is consequently is not limiting for soil microorganisms responsible for degrading the residues. However, Knapp *et al.* (1983) reported conflicting evidence where some studies found mixed results from the effect of N availability on residue decomposition.

Soil pH was fairly resilient to changes during the microcosm experiment (as clearly shown by PCA analysis) and this was actually not unexpected since it is not a highly variable parameter, and is often resilient also to short term perturbations (Table 3 and 4).

#### 1277 4.2 Soil biochemical properties

1278 This study confirms, as previously suggested (Ndiaye *et al.*, 2000), that biological and 1279 biochemical parameters are more sensitive and can provide earlier measurements of changes 1280 produced by different soil and crop management than physical and chemical indicators. Most 1281 authors have studied the quantity and the activity of soil microbial biomass as indicator of changes 1282 driven by the addition of organic residue or cropping systems (Kaiser and Heinemeyer, 1993; 1283 Ndiaye *et al.*, 2000).

Microbial biomass, is known to be one of the main drivers of nutrient cycling in soils, with microbial activity releasing essential nutrients to plants and microbial biomass is functionally and closely linked to the turnover of soil organic carbon (Jenkinson and Ladd, 1981). It is therefore of 1287 significance that the soil microbial biomass showed a greater increase, in all legume based 1288 treatments in the unamended soil. This increase, observed at the last sampling, could have been due to higher growth of microbial biomass, induced by the legume crop (Dinesh et al., 2004). The 1289 1290 statistically significant difference shown in the microbial biomass dynamics in response to the 1291 presence/absence of residues can depend on the decomposition rate of plant material and on the microbial immobilisation processes. In fact, the N assimilation requirements are determined by this 1292 1293 carbon flow (Mary et al., 1996). It is often assumed that N coming from the residue and from 1294 recycled biomass is mineralised before being assimilated by the newly-formed biomass. However, it 1295 has been shown that the soil microflora can directly assimilate significant amounts of organic N 1296 compounds coming from plant residues or from decaying biomass.

Furthermore, the introduction of the residue amendment increased soil basal respiration as measured by cumulative  $CO_2$  emissions. Although  $R_{bas}$  was not responsive to the individual treatments, it was markedly influenced by the interactions they determined with the amendment. This finding can suggest that in this soil the metabolic activity was primarily influenced by compositional changes in soil organic matter due an enhanced residue decomposition of the organic compounds released from plants roots.

#### 1303 *4.3 Analysis of soil microbial community structures*

The results obtained in this study confirm that the addition to the soil of crop residues can strongly modify the genetic structure of the community by stimulating particular populations; especially as the soil system is often substrate-limited as regards microbial growth (Nicolardot *et al.*, 2007). In fact, the molecular analysis revealed that the genetic structures of the bacterial population itself were significantly changed in response to the presence of legume sole crops or triticale, either in association with the legume or in monocropping, as a function of the presence/absence of wheat residue in the soils.

#### 1311 *4.4 Greenhouse Gas emissions*

1312 Our study demonstrated that there were lower N<sub>2</sub>O emissions from legumes, which is consistent 1313 with our understanding that there are low levels of N<sub>2</sub>O emission associated with the fixation 1314 process (Rochette and Janzen 2005). The results are also consistent with those of Pappa et al (2011) 1315 showing higher emissions from the pea cultivar Nitouche both as a monocrop and when grown as an intercrop. The Nitouche monocrop had up to six time higher emissions (434 g ha<sup>-1</sup>) than the 1316 monocrop Zero 4 (71 g ha<sup>-1</sup>) in the amended treatment and twice in the unamended (749 and 374 g 1317 ha<sup>-1</sup> for Nitouche and Zero 4, respectively). However, there was no significant difference between 1318 1319 the intercropping treatments. Intriguingly these higher emissions were observed in the absence of 1320 wheat residue additions, and did not appear to be associated with elevated concentrations of DOC. 1321 The denitrification processes driven by the availability of oxidisable carbon, which is used as a 1322 terminal electron acceptor in the respiratory process. Therefore, the absence of higher levels of DOC in the legumes was elevated emissions of N<sub>2</sub>O raises the possibility that the carbon was being 1323 1324 supplied by the legume itself. Support for this hypothesis would be provided by higher soil respiration rates measured from Nitouche, even in the absence of acid plant residues and as 1325 1326 indicated in differences in microbial activity shown by the ARISA analysis. There is also a growing 1327 body of evidence indicating that differences in rhizodeposition associated with different crop cultivars may drive differences in N2O emissions (Gogoi & Baruah 2012; Sey et al. 2010) 1328

1329 Plant species and combinations of species offer significant opportunities to modify soil derived 1330 N<sub>2</sub>O emissions. If differential rates of rhizodeposition are able to alter denitrification rates, then selecting specific legume cultivars with low rates of deposition in combination with cereals may 1331 1332 therefore provide a novel opportunity for the mitigation of N<sub>2</sub>O emissions. It is possible that the mechanisms underlying these differences would be associated either with an improved capacity of 1333 1334 certain legume cultivars to compete more efficiently for soil N. Alternatively there may be an 1335 interaction between the legume and soil microbial community that reduces N<sub>2</sub>O emission (possibly 1336 by promoting increased rates of N immobilization). The choice of legume cultivar and species is therefore a key factor influencing the amount of N loss. A previous study (Pappa et al., 2011) has 1337

1338 shown that the cultivar Zero 4 has significant lower N loss by  $N_2O$  emissions and leaching and 1339 could therefore contribute to the development of agricultural systems with environmental benefits. 1340 Therefore having a better understanding of the varietal differences in selecting intercrops mixtures 1341 has a high potential to increase yields and contribute towards the developments of agricultural 1342 systems with environmental benefits.

#### 1343 **5.** Conclusions

1344 Legumes are generally associated with lower emissions of N<sub>2</sub>O than cereal crops. However, 1345 there is significant variability in emissions between different legume cultivars. In this study the 1346 higher emissions associated with Nitouche were generated in the absence of wheat residues, raising the possibility that this variation in emissions is driven by variations in carbon supplied from the 1347 1348 legume root. The intercrop affect on microbial activity is also cultivar specific. This is indicated by differences in N<sub>2</sub>O emissions observed from two pea cultivars when grown as intercrops, although 1349 differences in N<sub>2</sub>O emission were not linked to differences in yield. The mechanism underlying 1350 1351 these differences appears to be driven by the differences resulting from microbial activity, which in 1352 turn are likely to be linked to soil-plant carbon dynamics.

1353 Our research therefore highlights the importance of the cultivar choice in the sustainable 1354 agricultural systems. The addition of the residues affects the soil C pools and the N<sub>2</sub>O emissions and 1355 shows clear differences between the two pea cultivars but also the intercropping combinations. The 1356 root development of pea monocrops was influenced by the residue addition but also the presence of 1357 cereal highlighting the complexity of such systems. The scale of these effects is highly sensitive to 1358 management and soil type. The growing need for environmental tests of the legume cultivars to understand further the mechanisms of the GHGs emissions is in high priority. Understanding the 1359 1360 development of legume cultivar and the interactions taking place within legume/cereal intercrop has 1361 the potential to be a very useful management tool in the development of more sustainable 1362 agricultural systems and in mitigation of GHG from agriculture.

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Table 1 – Chamber growth conditions during the 97-day experimental period were in accordance to
the 26-year average climatic data recorded between April and August in a Mediterranean
environment (Reggio Calabria, Southern Italy). The relative humidity was kept stable at 70%.
Lighting was produced by cool white fluorescent bulbs at an average intensity of 1160 lux.

Growth period (day)	Tempera	ture (°C)	Photoperiod (h)	
	Day	Night	Day/Night	
0-20	18.2 ± 0.3	10.2 ± 0.3	6.5/17.5	
21-40	23.4 ± 0.3	14.6 ± 0.2	8/16	
41-60	28.0 ± 0.3	18.9 ± 0.3	9.5/14.5	
61-80	30.6 ± 0.3	21.7 ± 0.2	10.5/13.5	
81-97	31.2 ± 0.4	22.5 ± 0.2	9.5/14.5	

1534	<b>Table 2</b> – Soil pH, EC, organic C and total N in the soil (mean $\pm$ SD, $n = 3$ ) was measured at the
1535	beginning and at the end of the experimental period. Symbols – and + represent absence or presence
1536	of amendment in soils. For each sampling time, different letters in the columns indicate significant
1537	differences among treatments (Tukey's HSD test at $P < 0.05$ ). Significant effects due to treatment,
1538	amendment, time and their interactions on the variability of data (F-value from three-way ANOVA,
1539	treatment x amendment x time, with corresponding $P$ values <sup>a</sup> ) are also shown at the bottom.

Treatment		pН	$\overline{EC_{1:2}}$ (dS m <sup>-1</sup> )	$C_{org}(mg g^{-1})$	$N_t (mg g^{-1})$
Nitoucho	-	6.19 ± 0.06	0.10 ± 0.01	34.13 ± 1.75	2.50 ± 0.10
Intouche	+	$6.24 \pm 0.07$	0.11 ± 0.01	29.94 ± 5.34	2.33 ± 0.29
7 4	-	6.17 ± 0.04	0.11 ± 0.01	34.13 ± 1.75	2.50 ± 0.10
Zero4	+	6.29 ± 0.03	0.11 ± 0.01	28.97 ± 4.41	2.33 ± 0.28
<b>1</b> Tuiting la	-	6.21 ± 0.04	0.10 ± 0.01	34.87 ± 0.92	2.53 ± 0.06
	+	6.23 ± 0.06	0.11 ± 0.01	30.07 ± 5.48	2.50 ± 0.20
	-	6.18 ± 0.04	0.10 ± 0.01	34.40 ± 0.26	2.53 ± 0.06
	+	$6.26 \pm 0.08$	0.11 ± 0.01	33.73 ± 1.60	2.60 ± 0.10
	-	6.19 ± 0.06	0.10 ± 0.01	33.83 ± 1.24	2.50 ± 0.10
Iriticale/Zero4	+	$6.24 \pm 0.07$	0.11 ± 0.01	33.47 ± 2.06	2.60 ± 0.11
	-	6.21 ± 0.04	0.11 ± 0.01	34.27 ± 1.76	2.53 ± 0.12
Bare soil	+	6.28 ± 0.03	0.11 ± 0.01	29.97 ± 5.58	2.50 ± 0.10
Nitoucho	-	6.31 ± 0.04 ª	$0.11 \pm 0.01^{b,c}$	36.36 ± 4.56	2.15 ± 0.02
Intouche	+	$6.25 \pm 0.03$	$0.12 \pm 0.01^{a,b}$	35.03 ± 7.51	2.12 ± 0.15
7 4	-	6.24 ± 0.04 <sup>a,b</sup>	0.10 ± 0.01°	32.19 ± 0.92	2.06 ± 0.03
Zero4	+	$6.27 \pm 0.04$	0.12 ± 0.02 <sup>b</sup>	37.54 ± 3.51	2.07 ± 0.01
	-	6.18 ± 0.03 <sup>a,b</sup>	$0.13 \pm 0.01^{a}$	30.32 ± 1.37	2.08 ± 0.06
	+	6.31 ± 0.03	0.10 ± 0.01 <sup>b</sup>	33.62 ± 2.31	2.05 ± 0.06
T.:	-	6.21 ± 0.03 <sup>a,b</sup>	$0.12 \pm 0.01^{a,b}$	36.96 ± 1.52	2.09 ± 0.10
Initicale/Nitouche	+	6.30 ± 0.03	0.11 ± 0.01 <sup>b</sup>	28.12 ± 2.12	1.87 ± 0.09
Tritical - 17 4	-	6.21 ± 0.02 <sup>a,b</sup>	$0.12 \pm 0.01^{a,b}$	34.62 ± 1.06	2.10 ± 0.01
Iriticale/Zero4	+	6.28 ± 0.07	$0.10 \pm 0.01$ b	30.58 ± 2.05	1.96 ± 0.19

Dana sail	-	6.16 ± 0.01 <sup>b</sup>	$0.10 \pm 0.01^{\circ}$	$30.98 \pm 0.43$	$2.09 \pm 0.07$
Bare son	+	6.29 ± 0.05	0.15 ± 0.01 <sup>a</sup>	28.89 ± 1.30	1.98 ± 0.32
Factor	df				
Treatment (T)	5	1.866 <sup>ns</sup>	1.866 <sup>ns</sup>	1.172 <sup>ns</sup>	0.510 <sup>ns</sup>
Amendment (A)	1	67.903***	67.903***	5.815 *	2.276 <sup>ns</sup>
Time (Ti)	2	5.026**	5.026**	2.238 <sup>ns</sup>	121.046 ***
ТхА	5	8.130***	8.130***	0.558 <sup>ns</sup>	0.146 <sup>ns</sup>
T x Ti	10	1.350 <sup>ns</sup>	1.350 <sup>ns</sup>	1.571 <sup>ns</sup>	1.204 <sup>ns</sup>
Ti x A	2	0.500 <sup>ns</sup>	0.500 <sup>ns</sup>	1.982 <sup>ns</sup>	16.213 ***
T x A x Ti	10	3.024**	3.024**	$2.897^{**}$	1.051 <sup>ns</sup>
Error	72				

Table 3 - Soil Principal component analysis (PCA) of 16 soil chemical and biochemical variables

1540 <sup>a</sup> Levels of significance: \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001; ns: not significant.

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measured in the six experimental treatments (Nitouche, Zero4, Triticale, Nitouche - Triticale, Zero4 - Triticale, Bare soil as in Materials and Methods) in the unamended soils during the 97-day microcosm experiment. PC loading variables (values  $\geq |0.60|$  are in bold) and percent of total variance explained by the first five factors (eigenvalue >1) are reported. Soil variables are as described in Materials and Methods.

Soil variable	PC1	PC2	PC3	PC4	PC5
PMN	-0.82	-0.32	-0.11	-0.06	-0.32
$N_t$	-0.82	-0.24	0.14	0.01	-0.13
R <sub>bas</sub>	0.82	0.15	-0.39	-0.18	-0.23
MBC/C <sub>org</sub>	0.80	-0.35	0.27	0.23	0.14
MBC	0.79	-0.34	0.34	0.11	0.14
$q\mathbf{M}$	0.75	0.07	-0.54	0.11	-0.15
DOC	0.73	0.34	0.28	0.07	0.11
C <sub>0</sub>	0.58	-0.07	-0.34	-0.23	-0.60
NH4 <sup>+</sup> -N	-0.01	0.83	0.06	-0.23	-0.19
qCO <sub>2</sub>	-0.24	0.78	-0.14	0.26	0.17
$q\mathrm{CO}_2/\mathrm{C}_{\mathrm{org}}$	-0.20	0.72	-0.27	0.37	0.13
MBN	0.37	0.01	0.70	0.12	-0.17

NO <sub>3</sub> -N	0.40	-0.45	-0.50	0.10	0.25
$\mathbf{C}_{\mathbf{org}}$	-0.01	0.13	0.49	-0.63	0.03
рН	0.09	0.15	0.45	0.60	-0.52
EC	0.48	0.44	0.17	-0.37	0.12
Variance explained (%)	33.55	17.44	13.54	8.43	6.63

**Table 4** – Principal component analysis (PCA) of 16 soil chemical and biochemical variables measured in the six experimental treatments (Nitouche, Zero4, Triticale, Nitouche - Triticale, Zero4 - Triticale, Bare soil as in Materials and Methods) in the amended soils during the 97-day microcosm experiment. PC loading variables (values  $\geq |0.60|$  are in bold) and percent of total variance explained by the first five factors (eigenvalue >1) are reported. Soil variables are as described in Materials and Methods.

Soil variable	PC1	PC2	PC3	PC4	PC5
MBC	0.92	-0.19	-0.01	-0.04	0.25
MBC/ C <sub>org</sub>	0.92	-0.18	-0.18	-0.05	0.16
qCO <sub>2</sub> / C <sub>org</sub>	-0.82	0.15	0.01	0.18	0.20
qCO <sub>2</sub>	-0.79	0.17	0.16	0.22	0.23
MBN	0.77	-0.27	-0.17	0.18	0.30
$\mathbf{N}_{\mathbf{t}}$	-0.77	-0.05	0.11	0.05	0.38
DOC	0.61	0.29	0.53	0.02	-0.07
PMN	-0.61	-0.28	-0.52	-0.26	0.26
R <sub>bas</sub>	0.36	0.83	-0.22	0.15	0.07
C <sub>0</sub>	0.09	0.78	-0.32	0.17	0.35
NO <sub>3</sub> -N	-0.01	-0.71	-0.18	0.56	-0.13
$q\mathbf{M}$	0.20	0.66	-0.59	0.06	-0.13
NH <sub>4</sub> <sup>+</sup> -N	-0.21	0.53	0.39	-0.20	-0.41
Corg	0.18	0.17	0.68	0.19	0.56
EC	-0.01	0.06	0.03	0.91	-0.28
рН	0.13	-0.07	0.48	-0.06	-0.02
Variance explained (%)	32.59	18.22	12.77	9.14	7.60

**Table 5** – Average above ground flux emissions ( $\mu$ g ml<sup>-1</sup>) for the whole experimental period for N<sub>2</sub>O, CO<sub>2</sub> and CH<sub>4</sub> followed by carbon dioxide equivalent, expressed in t, and then average below ground flux emissions ( $\mu$ g ml<sup>-1</sup>) for the whole experimental period for N<sub>2</sub>O, CO<sub>2</sub> and CH<sub>4</sub>. Symbols – and + represent absence or presence of amendment in soils. Significant effects due to treatment, amendment and their interaction on the variability of soil data (*F*-values from two-way ANOVA, treatment x amendment, with corresponding *P* values<sup>b</sup>) are also shown at the bottom.

Treatment			Above ground		Below ground		
	_	N <sub>2</sub> O	$CO_2$	CH <sub>4</sub>	N <sub>2</sub> O	CO <sub>2</sub>	CH <sub>4</sub>
Nitouche	-	$0.39 \pm 0.16^{b}$	1620.34 ± 1022.89	2.10 ± 0.81	$0.47 \pm 0.04^{\rm b}$	$2805.17 \pm 639.15^{b}$	2.34 ± 0.13
Witouche	+	0.38 ± 0.10	2253.45 ± 1608.46	$2.10 \pm 0.78$	$0.59 \pm 0.12^{b}$	$5075.28 \pm 701.74^{b}$	$2.17 \pm 0.11^{b}$
Zerol	-	$0.33 \pm 0.11^{b}$	2076.57 ± 1869.64	2.07 ± 0.81	$0.66 \pm 0.11^{b}$	4386.84 ± 719.72 <sup>b</sup>	2.00 ± 0.14
20104	+	$0.34 \pm 0.09$	2219.74 <b>±</b> 1795.18	$2.06 \pm 0.86$	$0.72 \pm 0.15^{b}$	$7073.73 \pm 992.48^{b}$	$2.05 \pm 0.14^{b}$
Triticale	-	$0.59 \pm 0.55^{a,b}$	2077.48 ± 1704.66	2.12 ± 0.51	$2.08 \pm 1.00^{b}$	3048.84 ± 447.91 <sup>b</sup>	2.12 ± 0.15
Inteac	+	0.37 ± 0.15	2156.48 ± 1722.16	2.14 ± 0.86	$0.56 \pm 0.08^{b}$	$10373.01 \pm 1115.54^{b}$	$2.26 \pm 0.09^{b}$
Triticale/Nitouche	-	$0.86 \pm 0.38^{a}$	1920.04 ± 1616.19	$2.35 \pm 0.67$	$2.56 \pm 1.17^{b}$	7799.00 ± 1167.89 <sup>b</sup>	2.10 ± 0.14
Thicale/Wilducke	+	0.30 ± 0.11	2243.43 ± 1870.47	$2.05 \pm 0.86$	$1.30 \pm 0.42^{a,b}$	7714.24 ± 1584.48 <sup>b</sup>	$2.29 \pm 0.09^{b}$
Triticale/ZeroA	-	$0.38 \pm 0.07^{a,b}$	2054.57 ± 1878.98	2.11 ± 0.78	$0.87 \pm 0.33^{b}$	$3725.17 \pm 415.45^{b}$	2.23 ± 0.12
	+	0.36 ± 0.10	2388.89 ± 2103.67	$2.07 \pm 0.82$	$0.67 \pm 0.14^{\rm b}$	$7743.60 \pm 683.45^{b}$	$2.18 \pm 0.12^{b}$
Dare sail	-	$0.80 \pm 0.33^{a,b}$	1687.66 ± 1205.27	$2.17 \pm 0.73$	$19.70 \pm 4.76^{a}$	7907.47 ± 1193.37 <sup>a</sup>	2.31 ± 0.16
Bare son	+	$0.36 \pm 0.08$	2389.69 ± 2266.00	2.14 ± 0.89	$1.95 \pm 0.37^{a}$	$17480.05 \pm 1398.95^{a}$	$3.28 \pm 0.37^{a}$
Factor	df						
Treatment (T)	5	3.286 **	0.050 <sup>ns</sup>	0.062 <sup>ns</sup>	12.008 ***	14.550 ***	4.173 **
Amendment (A)	1	18.408 ***	1.064 <sup>ns</sup>	0.141 <sup>ns</sup>	13.033 **	44.209 ***	3.216 <sup>ns</sup>
ТхА	5	4.116 **	0.083 <sup>ns</sup>	0.093 <sup>ns</sup>	9.221 ***	5.023 ***	2.374 *
Error	84						

1560 <sup>a</sup> Different letters in a column indicate significant differences among treatments (Tukey's test at P < 0.05). <sup>b</sup> Levels of significance: \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001; ns: not significant.

**Table 6** – Emission intensities (total cumulative N<sub>2</sub>O measurements divided by the total biomass for the whole experimental period), expressed in g per t of total biomass. Symbols – and + represent absence or presence of amendment in soils. Significant effects due to treatment, amendment and their interaction on the variability of soil data (*F*-values from twoway ANOVA, treatment x amendment, with corresponding *P* values<sup>b</sup>) are also shown.

Treatment		Intensities						
Incutinent		N <sub>2</sub> O	CO <sub>2</sub>	CH <sub>4</sub>				
Nitouche	-	0.04 ± 0.41	219.30 ± 302.67	171.22 ± 62.25				
Nitouene	+	$0.01 \pm 0.04$	933.45 <b>±</b> 258.87	143.11 ± 98.77				
Zarol	-	0.92 ± 0.33	1066.66 ± 201.18	182.58 ± 153.10				
Ze104	+	$-0.02 \pm 0.48$	1119.81 <b>±</b> 647.68	58.53 ± 175.01				
Triticale	-	1.33 ± 0.84	898.48 ± 789.79	199.41 ± 310.07				
Inticale	+	-0.11 ± 0.36	1159.32 ± 256.00	462.84 ± 691.76				
Triticale/Nitouche	-	0.68 ± 1.15	774.83 ± 1465.21	166.11 ± 167.84				
Introde / Nitouche	+	0.24 ± 0.35	2104.40 ± 1861.08	543.02 ± 879.48				
Triticala/Zana 4	-	$0.18 \pm 0.40$	846.15 ± 47.80	355.79 ± 44.58				
Inucale/Zero4	+	-0.30 ± 0.31	1492.26 ± 1035.41	180.94 ± 409.14				
Factor	df							
Treatment (T)	4	1,754 <sup>ns</sup>	0,603 <sup>ns</sup>	0,566 <sup>ns</sup>				
Amendment (A)	1	8,884 **	2,008 <sup>ns</sup>	0,098 <sup>ns</sup>				
ТхА	4	2,463 <sup>ns</sup>	0,219 <sup>ns</sup>	0,462 <sup>ns</sup>				
Error	18							

1566 <sup>a</sup> Different letters in a column indicate significant differences among treatments (Tukey's test at P < 1567 = 0.05).

1568 <sup>b</sup> Levels of significance: \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.001; ns: not significant.

#### **Figure captions**

1572 **Fig. 1.** Changes in soil dissolved organic C (DOC), basal respiration ( $R_{bas}$ ), potential 1573 mineralisable C ( $C_0$ ) and microbial biomass C (MBC) (mean ± SD, n=3) in unamended (left)

- and amended (right) microcosm soils at three sampling times (0, 62 and 97 DAS) over the 97-
- day experimental period for the six treatments: Nitouche, Zero4, Triticale, Triticale-Nitouche,
  Triticale-Zero4, bare soil.

1577 **Fig. 2.** Changes in KCl-extractable ammonium-N (NH<sub>4</sub><sup>+</sup>-N), KCl-extractable nitrate-N (NO<sub>3</sub><sup>--</sup>

1578 N), potential mineralisable N (PMN) and microbial biomass N (MBN) (mean  $\pm$  SD, n=3) in

unamended (left) and amended (right) microcosm soils at three sampling times (0, 62 and 97
DAS) over the 97-day experimental period. Treatments are as in Fig. 1.

1581 Fig. 3. Changes in mineralization coefficient (qM), metabolic quotient ( $qCO_2$ ),  $qCO_2/C_{org}$ 

1582 ratio and microbial quotient (MBC/C<sub>org</sub>) (mean  $\pm$  SD, n=3) in unamended (left) and

amended (right) microcosm soils at three sampling times (0, 62 and 97 DAS) over the 97-day
experimental period. Treatments are as in Fig. 1.

**Fig. 4.** PCA ordination biplot (PC1 *vs* PC2) of 16 soil chemical and biochemical variables (loadings, see Materials and Methods) measured in the six experimental treatments (Nitouche, Zero4, Triticale, Triticale-Nitouche, Triticale-Zero4, bare soil as in Materials and Methods) (scores) at three sampling times (pre-sowing, flowering, harvest) in the unamended (A) and the amended soils (B) during the 97-day microcosm experiment. The biplot has the same origin for scores and loadings.

1591 Fig. 5. Hierarchical classification (Pearson's similarity coefficient, Ward's clustering method)

1592 of banding patterns generated by ARISA of PCR-amplified 16S rRNA gene-coding fragments

1593 from soil-extracted bacterial DNA from no-residue (A) and residue (B) added microcosms at

two sampling times (62 and 97 DAS) over the 97-day experimental period. Treatments are as
in Fig. 1. Each bar averages three microcosm replicates. Scale bar (0–100) indicates the
similarity level.













1608 Figure 5 (ARISA analysis)

